

Input file F1h14273new; Output File F1h14273tra
Sequence length 1743

TCGGGACTAGTTCTAGACCGCTGGGGCCAGGGGGAA ATG TCC CCT GAA TGC GCG CGG GCA GCG 9
G D A P L R S L E Q A N R T R F P F C A R A A 27
GGC GAC GCG CCC TTG CGC AGC CTG GAG CAA GCC AAC CGC ACC CGC TTT CCC TTC TCC S 29
D V K G D H R L V L A A V E T T V L V L 87
GAC GTC AAG GGC GAC CAC CGG CTG GTG CTG GCC GCG GTG GAG ACA ACC GTG CTG GTG CTC 147
I F A V S L L G N V C A L V L V A R R R 49
ATC TTT GCA GTG TCG CTG CTG GGC AAC GTG TGC GCC CTG GTG CTG GTG GCG CGC CGA CGA 207
R R G A T A C L V L N L F C A D L L F I 69
CGC CGC GGC GGC ACT GCC TGC CTG GTC CTC AAC CTC TTC TGC GCG GAC CTG CTC TTC ATC 267
S A I P L V L A V R W T E A W L L G P V 109
AGC GCT ATC CCT CTG GTG CTG GCC GTG CGC TGG ACT GAG GCC TGG CTG CTG GGC CCC GTT 327
A C H L F Y V M T L S G S V T I L T L 129
GCC TGC CAC CTG CTC TAC GTG ATG ACC CTG AGC GGC AGC GTC ACC ATC CTC ACG CTG 387
A A V S L E R M V C I V H L Q R G V R G 149
GCC GCG GTC AGC CTG GAG CGC ATG GTG TGC ATC GRG CAC CTG CAG CGC GGC GTG CGG GGT 447
P G R R A R A V L G L Q R G V R G 169
CCT CGG CGG CGG GCA GTC CTG GCG CTC ATC TGG GCC TAT TCG GCG GTC GCC 507
A L P L C V F F R V P Q R L P G A D Q 189
GCT CCT CTC TGC GTC TTT CGA GTC CGG CAA CGG CTC CCC GGC GAC CAG 567

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TO FIG. 1B.

FIG. 1A.



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FROM FIG. 1A.

E	I	S	I	C	T	L	I	W	P	T	I	P	G	E	I	S	W	D	V	209	
GAA	ATT	TCG	ATT	TGC	ACA	CTG	ATT	TGG	CCC	ACC	ATT	CCT	GGG	GAG	ATC	TCG	TGG	GAT	GTC	627	
S	F	V	T	L	N	F	L	V	P	G	L	V	I	V	I	S	Y	S	K	229	
TCT	TTT	GTT	ACT	TTC	TTC	TTC	TTC	TTC	GTC	CCA	GGG	CTG	GTC	ATT	GTG	ATC	AGT	TAC	TCC	AAA	687
I	L	Q	I	T	K	A	S	R	K	R	L	T	V	S	L	A	Y	S	E	249	
ATT	TTA	CAG	ATC	ACA	AAG	GCA	TCA	AGG	AAG	AGG	CTC	ACC	GTA	AGC	CTG	GCC	TAC	TCG	GAG	747	
S	H	Q	I	R	V	S	Q	D	F	R	L	F	R	T	L	F	L	L	L	269	
AGC	CAC	CAG	ATC	CGC	GTG	TCC	CAG	GAC	TTC	CGG	CTC	TTC	CGC	ACC	CTC	CTC	CTC	CTC	CTC	807	
M	V	S	F	F	I	M	W	S	P	I	I	T	I	L	L	I	L	I	I	208	
ATG	GTC	TCC	TTC	TTC	ATC	ATG	TGG	AGC	CCC	ATC	ATC	ATC	ACC	ATC	CTC	CTC	CTC	ATC	CTG	ATC	867
Q	N	F	K	Q	D	L	V	I	W	P	S	L	F	F	W	V	V	A	F	309	
CAG	AAC	TTC	AAG	CAA	GAC	CTG	GTC	ATC	TGG	CCG	TCC	CTC	TTC	TTG	GTG	GTG	GCC	TTC	927		

TO FIG. 1C.

FIG. 1B.



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FROM FIG. 1B.

T	F	A	N	S	A	L	N	P	I	L	Y	N	M	T	C	R	N	E	329	
ACA	TTT	GCT	AAT	TCA	GCC	CTA	AAC	CCC	ATC	CTC	TAC	AAC	ATG	ACA	CTG	TGC	AGG	AAT	GAG	987
W	K	K	I	F	C	C	F	W	F	P	E	K	G	A	I	L	T	D	T	349
TGG	AAG	AAA	ATT	TTT	TGC	TGC	TTC	TGG	TTC	CCA	GAA	AAG	GGA	GCC	ATT	TAA	ACA	GAC	ACA	1047
S	V	K	R	N	D	L	S	I	I	S	G	•	362							
TCT	GTC	AAA	AGA	AAT	GAC	TTC	TGG	ATT	ATT	TCT	GGC	TAA	1086							

TTTTCTTTAAGCCGAGTTCTCACACCTGGGAGCTGGCATGGCTTTAAACAGAGTTCAATTCCAGTACCCCTCCA
 TCAGTGACCCCTGCTTTAAGAAAATGAAACCTATGCAAATAGACATCCACAGCTCGGTAAATTAAAGGGGTGATCACCAA
 GTTTCATAATAATTCCCTTTATAAAAGGATTGGCCAGGTGCAGTGGTTCATGCCTGTAATCCCAGCAGTTGGG
 AGGTGAGGTGGTGGATCACCTGAGGTCAAGGTTGAGGTTGAGGTTGAGGAACTGACCAACATGGTAGACCCCCGCTCTACTA
 AAAATAAAAAAAATTAGCTGGGAAGTGGTGGGCACCTGTAATCTAGCTACTTGGAGGCTGAACCAGGAAAT
 CTCTGAACCTGGGAGGCAAGGGTGCAGTGAAGCCAGATCGTGCCTAAACCCAGGGCAACAAAGAGTGAAC
 TCCATCTTAAAGGGTTATGGTTAATGTAACCTTTAGTGTGTTGTAATATG
 ATCAAATTAATAATATTATGACTGTTAGCAAGAAAAAAAGGGCGG

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FIG. 1C.

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Sequence	Description	score	E-value	N
7tm_1	PF00001 7 transmembrane receptor (rhodopsin)	119.9	4.7e-37	1

Parsed for domains:

Sequence	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value	-
7tm_1	1/1	57	321	1	259	[]	119.9	4.7e-37

Alignments of top-scoring domains:

7tm_1: domain 1 of 1, from 57 to 321: score 119.9, E = 4.7e-37

```

*->GN1LVi1vi1rtkki1rtptni1i1LAVADLLf11t1ppw1yyy1vg
      GN+ ++++++r +++r +t +++INL ADLLF + p++ ++ -+

```

F1h14273, 57 GNVCALVLVAR-RRRRGATACLVNLFCADLLFISA1PLVLAVR-WT 101

```

gaadWpfGsa1Ck1vtaldvvnmyaSi11Lta1SiDRY1A1vhP1ryrrr
      e W++G++ C+1+ +++++++ + i1+L+a S++R + Iv 1+ +r

```

F1h14373, 102 --EAWLLGPVACHLLFYMTLSGSVTILTAAVSLERMVCIV-HLQRGVR 148

```

rtsprAkvvi11vvv1a111si1Pp11fsw1ktveegngt1nvnevCi
      +r +v++1+W +++++1P +f+ v+ ++ ++ ++ +C+++

```

F1h14273, 149 GPGRRARAVLLALIWGYSAVAALPLCVFFRVPQRPG--ADQEISICTL 196

```

dfpccstasvstw1rsyvv11stwgF11Pp11vi1vcYtri1rtr.....
      +p++++ +ts+ ++ ++ F1+P 1v++ Y+ II + + ++++

```

F1h14273, 197 IWPT1PG--E1SWDVSFVTLNLFYRGLVIVJSYSKILQITKasrkr 240

```

.....kaakt11vvvvFv1CW1Pyfiv111dt1c
      + + +++++ + +++++ ++ +t1++++v F++ W P i++11 +

```

F1h14273, 241 1cv51oyseehq1rvsqqdfRLFRTLFLMVSFFIMWSPIIITILLILQ 290

```

.1s11msstCelervpta11vtwLayvNsc1NP11Y<-*+
      + + + + p++++ + +++++Na+1NP1+Y

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F1h14273, 291 nFK-----QDLVIWPSLFFVVVAPTFANSALNPILY 321

FIG. 2.



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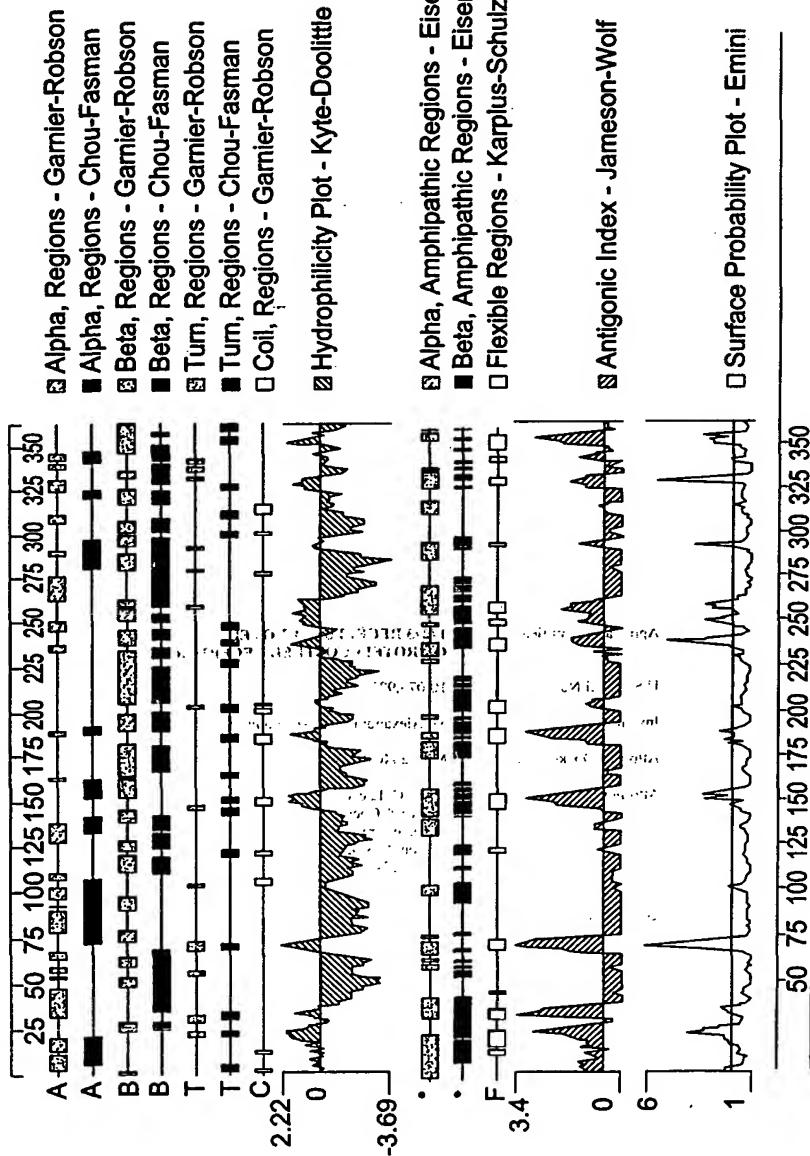


FIG. 3.

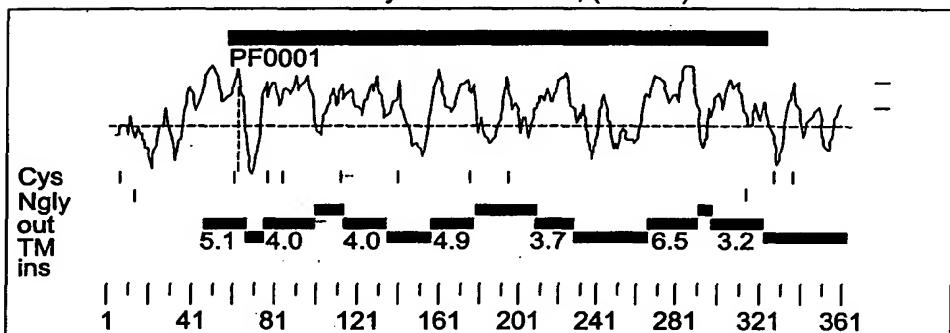
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Analysis of Flh14273, (362 aa)



>Flh14273, 1086 bases, 1825 checksum.
MSPECARAQQDAPLRSLEQANRTRFPFFSDVKGDHRLVLAAVETTVLVL
LEFAVSLLGNVC
ALVLVARRRRRGATAQLVNLFCADLLFYSAIPLVLA
VWTEAVLLGPVACHLLFYVMTL
SGSVTILTAAVSLERMVCIVHLQRCVRGPGRARRAVLLALIWGY
SAVAALPLCVFFRVV
PQR LP GADQEISICTLIWPTIPGEISWDSFVTLNFLVPG
L VIVISYSKILQITKASRKR
LTVSLAYSESHQIRVSQQDFRLFRFLMVSFFIWWSPII
TILLIQLQNFKQDLV
IWP
SLFFVVVAFTFANSALNPILYNM
TLCRNEWKKIFCCFWFGPEKG
AILTDSVKRNDLSIIS
G+

FIG. 4.



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Prosite Pattern Matches for F1h14273

>PS00001/P00C0001/ASN_GLYCOSYLATION N-glycosylation site.

Query: 21 NRTR 24
Query: 322 NMTL 325

>PS0004/P00C0004/CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.

Query: 239 KRLT 242

>PS0005/P00C0005/PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 237 SRK 239
Query: 350 SVK 352

>PS0006/P00C0006/CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 256 SQQD 259

>PS00008/P00C0008/MYRISTYL N-myristoylation site.

Query: 57 GNVCAL 62
Query: 72 GATACL 77
Query: 343 GAILTD 348

>PS00009/P00C0009/AMIDATION Amidation site.

Query: 150 PCRR 153

>PS00029/P00C00029/LEUCINE_ZIPPER Leucine zipper pattern.

Query: 106 LGPVACHLLFYVMTLSGSVTL 127

FIG. 5.



Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
46	66	out->ins	5.1
75	98	ins->out	4.0
113	134	out->ins	4.0
156	177	ins->out	4.9
209	227	out->ins	3.7
266	289	ins->out	6.5
297	321	out->ins	3.2

>F1h14273,

MSPECARAAGDAPLRSLEQANRTRFPFFSDVKGDHRLVLAAVETTVLVLIPAVSLLGNVC
 ALVLVARRRRRGATACLVNLFCADLLFISAWPLVLAVRWTEAWLLGPVACHLLFYVMTL
 SGSVTILTAAVSLERMVCIVHLQRGVRGPGRRARAVLLALIWGYSAVAALPLCVFFRVP
 PQRLPGADQEISICTLIWPTIPGEISWDVSFVTLNFLVPGLVIVVISYSKILQITKASRKR
 LTVSLAYSESHQIRVSQQDFRLFRTLFLMVSFFIMWSPIIITILLIIQNFKQDLVIWP
 SLFFFVVVAFTFANSALNPILYNMTLCRNEWKKIFCCFWFPEKGAILTDTSVKRNDLSIIS
 G

Transmembrane Segments for Presumed Mature Peptide

Start	End	Orient	Score
14	37	ins->out	4.0
52	73	out->ins	4.0
95	116	ins->out	4.9
148	166	out->ins	3.7
205	228	ins->out	6.5
236	260	out->ins	3.2

>F1h14273, _mature

LVLVARRRRRGATACLVNLFCADLLFISAIPLVLAVRWTEAWLLGPVACHLLPYVMTLS
 GSVTILTAAVSLERMVCIVHLQRGVRGPGRRARAVLLALIWGYSAVAALPLCVFFRVP
 QRLPGADQEISICTLIWPTIPGEISWDVSFVTLNFLVPGLVIVVISYSKILQITKASRKR
 LTVSLAYSESHQIRVSQQDFRLFRTLFLMVSFFIMWSPIIITILLIIQNFKQDLVIWP
 LFFFVVVAFTFANSALNPILYNMTLCRNEWKKIPCCFWFPEKGAILTDTSVKRNDLSIISG

FIG. 6.



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Input file 14273m, Output File 14273mra
Sequence length 1560
TTGCCAAGCTAGGGTAAGCCTCTTCCACTGCAATCTCACAGAAGGGTTCATGGAGTGCTCACACCATCAGTGACCA

CTCAGACTTGTCCGGCTTACCCGAATCTCACAGGGAGTCGATGACCCCTCTGACAGGCCACGAGGGCGGCAGGCT	M	S	P	E	C	A	Q	T	T	G	10
CGCCATCTTGGGACGGTGGGGGGGGGGCGGC	ATG	TCC	CCT	GAG	TGT	GCA	CAG	ACG	ACG	GGC	30
P	G	P	S	H	T	L	Q	V	N	R	10
CCT	GCT	CCC	TCG	CAC	ACC	CTG	GAC	CGA	AAT	CGC	30
V	K	G	D	H	R	L	V	S	V	E	10
GTC	AAG	GGC	GAC	CAC	CGG	TG	GTC	GAG	ACC	ACC	50
F	V	V	S	L	T	TG	N	Y	C	A	150
TTT	GTC	GTC	TCA	CTG	CTG	GGC	AAC	GGG	TGT	CTA	150
R	G	A	S	A	S	TG	CTG	CTG	GTC	GTC	70
CGT	GGG	GCG	TCA	GCC	AGC	CTG	GTG	CTC	AAC	CTC	210
A	I	P	L	V	L	V	R	V	T	C	90
GCC	ATC	CCT	CTA	GTG	CTC	GTC	GTG	GTC	GAT	TTC	270
C	H	L	L	F	Y	M	M	M	A	D	130
TGC	CAC	CTG	CTG	CTC	TAC	GTG	ATG	ACA	ATG	AGC	390
A	V	S	L	E	R	M	V	C	I	V	130
GCG	GTC	AGC	CTG	GAG	CGC	ATG	GTG	TGC	ATC	GTG	390
G	R	R	T	Q	A	L	A	F	I	W	150
GGG	CGG	CGG	ACT	CAG	GCG	GGC	CTG	GCT	TTC	ATA	450
										A	170
										GGC	510

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TO FIG. 7B.

FIG. 7A.

FROM FIG. 7A.

L P L Y I L F R V V P Q R L P G G D Q E 192
 CTC CCC CTC TAC ATC TTT GTC CGC GTC CCG CAG CTC CCC GGC GAC CAG GAA 62
 I P I C T L D W P N R I G E I S V F 210
 ATT CCG ATT TGC ACA TTG GAT TGG CCC AAC CGC ATA GGA GAA ATC TCA TGG GAT GTG TTT 630
 F E T L N F L V P G L V I V I S Y S K I 230
 TTT GAG ACT TTG AAC TTC CTG GTG CGC ATT GTG ATC AGT TAC TCC AAA ATT 690
 L Q I T K A S R K R L T L S L A Y S E S 250
 TTA CAG ATC ACG AAA GCA TCG CGG AGG CTC ACG CTC AGC TTG GCA TAC TCT GAG AGC 750
 H Q I R V S Q Q D Y R L F R T L F L M 270
 CAC CAG ATC CGA GTG TCC CAA CAA GAC TAC CGA CTC TTC CGC AGC CTC TTC CTC ATC ATC 810
 V S F F I M W S S P I I T I L L I L Q 290
 GTT TCC TTC ATC ATG TGG AGT CGC ATC ATC ACC ATC CTC CTC ATC TTG ATC CAA 870
 N F R Q D V I P S L F F W V V A F T 310
 AAC TTC CGG CAG GAC CTG GTC ATC TGG CCA TCC CTT TTC TCC TGG GTG GCC TTC ACG 930
 F A N S A L N P I L Y N M S L F R N E W 330
 TTT GCC AAC TCT GCC CTA AAC CCC ATA CTG TAC AAC ATG TCG TCT AGG AAC GAA TGG 990
 R K I F C C E F P E K G A I F T D T S 350
 AGG AAG ATT TTT TGC TGC TTC ATT CCA GAG AAG GGA GCC ATT TTT ACA GAT ACG TCT 1050
 V R R N D L S V S S • 362
 GTC AGG CGA AAT GAC TTG TCT GTT ATT TCC AGC TAA 1086

CTAGCCTCTGGTGCAGGTGAACCAAGGTGATGTTAAAGCGAGTTAACTTCAAGGAAAGCCACCAAGGTGCGCCCTGC
 TTTAAAAATAACCGACTTCAACAGCAGGGCATCTACGGAGGCCATTAAAGGAATGATCGCTCAGTATAAAATATT
 TTTCTTAAAGAACCTTCTATGGGTTCTTTGTGAACCTTTTAAGTGTGTAAATATGATCTAGTTAATAAAATT
 TTTATTTATAACGTGTTCTACAAAAAAACAAAAAA

FIG. 7B.

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A circular stamp with the word 'OIPE' at the top, 'SANTO DOMINGO' on the right, 'PATENT & TRADEMARK OFFICE' at the bottom, and the date 'JUL 22 2002' in the center.

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Query: 14273m,

Scores for sequence family classification (score includes all domains):

Sequence	Description	Score	E-value	N
7tm_1	PF00001 7 transmembrane receptor (rhodopsin	118.8	1e-35	1

Parsed for domains!

Sequence	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
7tm 1	1/1	57	321 ..	1	259 []	118.8	1e-36

Alignments of top-scoring domains:

7tm_1: domain 1 of 1, from 57 to 321: score 118.8, E = 1e-36

*->GN1LV1v1r1t1k1r1t1p1t1n1f11NL1AvAD1L1f11t1p1p1w1y1v1g
GN1t1t1t1t1r1t1t1r1t1t1t1N1L1AD1L1f1t1p1t1t1t1t1

14273m, 57 GNV CAL VL VAR-RRRRGASASLVLNLFCADLLFTSAIPLVLVVR-WT 101

gaadWpfGaa1Ck1vt1dvvnmyaS111Lta1S1DRY1A1vhP1ryrrr
e W++G++C+1+ +++++++ + 11+L+a S++R + Iv 1r +

14273m, 102 --EAWLLGPVVCHLLPYVMTMSGVTLTLAAVSLERMVCIV-RLRRGLS 148

rtsprrA.kvv;11vWv1a111s1Pp11fswvktveagngt1nvntvC1
rr++++++W ++1++1P +++++ v + ++q ++ +C+

14273m, 149 GP-GRRTqAALLAFIWGYSAALALPLYILFRVVPQRLLPGGD--QEITPCT 195

14273m. 196 LDWPNRIG-----EISWDVFFETLNFLVPGLVIVISYSKILQITKasrk 239

14273m 240 r1t1s1ayseshairvsadlyRI FRTI F11 MVSF1 PMVSPI TTTTTT T11 1289

14373-380 OnEP-----ODLVIVPSLEFHVVAFTEANSAINRILY 321

FIG. 8.



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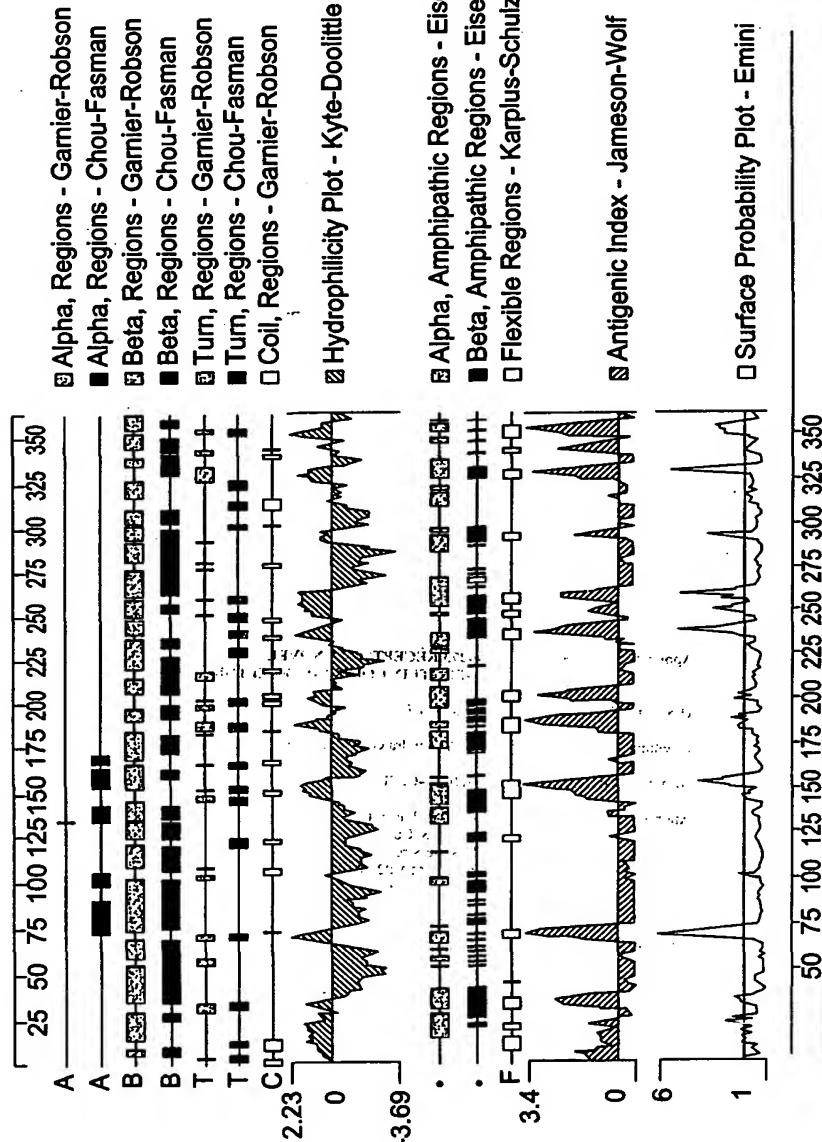


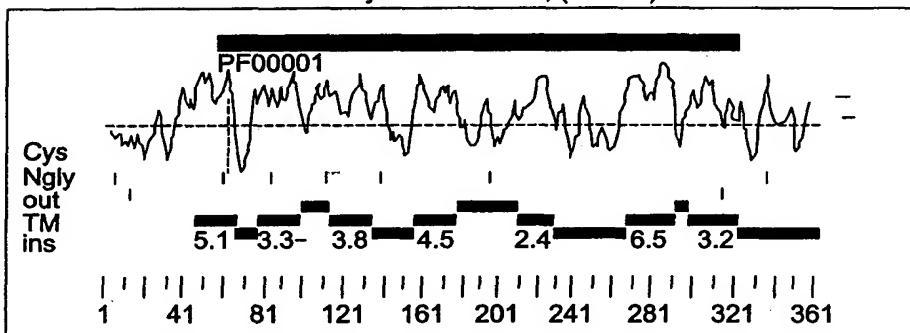
FIG. 9.



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Analysis of 14273m, (362 aa)



>14273m, 1086 bases, 6943 checksum.
 MSPECACOTTGCPGPSHTLDQVNRTTHFPFFSDVKGDHRLVLSVVETTVLGLIFVVSLLGNVC
 ALVLVARRRRRGASASLVNLFCADLLFTSAIPLVLVVRWTEAWLLGPVVCCHLLFVVMTC
 SGSVTILTLAAVSLERMVCIVRLRRGLSGPGRRTQAALLAFIWGYSALAALPLYILFRVV
 PQRLPGGDQEIPICTLDWPNRIGEISWDVFFETLNFLVPGLVIVISYSKILQITKASRKR
 LTLSLAYSESHQIRVSQQDYRLFRTLFLMVSFFIWSPIIIITILLIIONFRQDLVIWP
 SLFFFVVVAFTFANSALNPILYMSLFRNEWRKIFCCFPPEKGAIFTDTSVRRNDLSVIS
 S*

FIG. 10.



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Prosite Pattern Matches for 14273m,

>PS00001/PDDC00001; ASN_GLYCOSYLATION N-glycosylation site.

Query: 21 NRTH 24
Query: 322 NRTH 325

>PS00002/PDDC00002; GLYCOSAMINOGLYCAN Glycosaminoglycan attachment site.

RU Additional rules:
RU There must be at least two acidic amino acids (Glu or Asp) from -2 to -4 relative to the serine.
Query: 148 SGPG 151

>PS00004/PDDC00004; cAMP- and cGMP-dependent protein kinase phosphorylation

Query: 239 KRLT 242

>PS00005/PDDC00005; PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 237 SRK 239
Query: 350 SVR 352

>PS00006/PDDC00006; CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 40 SVVE 43
Query: 256 SQQD 259

>PS00008/PDDC00008; MYRISTYL N-myristoylation site.

Query: 57 GNVCAL 62
Query: 72 GASASL 77
Query: 343 GAIFTD 348

>PS00009/PDDC00009; AMIDATION Amidation site.

Query: 150 PGRR 153

FIG. 11.



Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
46	66	out->ins	5.1
77	98	ins->out	3.3
113	134	out->ins	3.8
156	177	ins->out	4.5
209	227	out->ins	2.4
266	289	ins->out	6.5
297	321	out->ins	3.2

>14273m,

MSPECAGTTGPGPSHTLDQVNRTHFPPFSDVKGDHRLVLSVVEETVLGLIFVVSLLGNVC
 ALVLVARRRRRGASASLVLNLFCADLLFTSAIPLVLVVRWTEAWLLGPVVCCHLLFYVMTM
 GSVTILTAAVSLERMVCIVRLRRGLSGPGRRTQAALLAFIWGYSALAALPLYILFRVV
 PQRLPGGDQEIPICLTDWPNRIGEISWCVFFETLNFLVPGLVIVISYSKILQITKASRKR
 LTLSLAYSESHQIRVSQQDYRLFRTLFLMVSFFIMWSPIIITILLILIQNFRQDLVIWP
 SLFFWVVAFTFANSALNPILYMMMSLFRNEWRKIFCCFFFPEKGAIIFTDTSVRRNDLSVIS
 S

Transmembrane Segments for Presumed Mature Peptide

Start	End	Orient	Score
16	37	ins->out	3.3
52	73	out->ins	3.8
95	116	ins->out	4.5
148	166	out->ins	2.4
205	228	ins->out	6.5
236	260	out->ins	3.2

>14273m, _mature

LVLVARRRRRGASASLVLNLFCADLLFTSAIPLVLVVRWTEAWLLGPVVCCHLLFYVMGMS
 GSVTILTAAVSLERMVCIVRLRRGLSGPGRRTQAALLAFIWGYSALAALPLYILFRVVP
 QRLPGGDQEIPICLTDWPNRIGEISWCVFFETLNFLVPGLVIVISYSKILQITKASRKR
 LTLSLAYSESHQIRVSQQDYRLFRTLFLMVSFFIMWSPIIITILLILIQNFRQDLVIWP
 LFFWVVAFTFANSALNPILYMMMSLFRNEWRKIFCCFFFPEKGAIIFTDTSVRRNDLSVIS

FIG. 12.